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#2



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## RAW SEQUENCE LISTING

DATE: 03/19/2002

PATENT APPLICATION: US/09/824,647

TIME: 14:49:08

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Output Set: N:\CRF3\03192002\I824647.raw

1 <110> APPLICANT: Serrero, Ginette  
 2 <120> TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS  
 3 <130> FILE REFERENCE: Z9996.488/P001-A  
 4 <140> CURRENT APPLICATION NUMBER: 09/824,647  
 5 <141> CURRENT FILING DATE: 2001-04-04  
 7 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862  
 W--> 8 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17  
 11 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862  
 W--> 12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23  
 13 <160> NUMBER OF SEQ ID NOS: 17  
 14 <170> SOFTWARE: PatentIn Ver. 2.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 2137  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Mouse epithelin/granulin  
 20 <220> FEATURE:  
 21 <221> NAME/KEY: CDS  
 22 <222> LOCATION: (23)..(1789)  
 23 <223> OTHER INFORMATION: The sequence is identical to that of the published  
 24 mouse granulin except for one nucleotide (T  
 25 instead of G) at position 1071 of GP88 cDNA  
 26 (position 1056 of mouse granulin).  
 27 <400> SEQUENCE: 1  
 28 cggacccccga cgcagacaga cc atg tgg gtc ctg atg agc tgg ctg gcc ttc 52  
 29 Met Trp Val Leu Met Ser Trp Leu Ala Phe  
 30 1 5 10  
 31 gcg gca ggg ctg gta gcc gga aca cag tgt cca gat ggg cag ttc tgc 100  
 32 Ala Ala Gly Leu Val Ala Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys  
 33 15 20 25  
 34 cct gtt gcc tgc tgc ctt gac cag gga gga gcc aac tac agc tgc tgt 148  
 35 Pro Val Ala Cys Cys Leu Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys  
 36 30 35 40  
 37 aac cct ctt ctg gac aca tgg cct aga ata acg agc cat cat cta gat 196  
 38 Asn Pro Leu Leu Asp Thr Trp Pro Arg Ile Thr Ser His His Leu Asp  
 39 45 50 55  
 40 ggc tcc tgc cag acc cat ggc cac tgt cct gct ggc tat tct tgt ctt 244  
 41 Gly Ser Cys Gln Thr His Gly His Cys Pro Ala Gly Tyr Ser Cys Leu  
 42 60 65 70  
 43 ctc act gtg tct ggg act tcc agc tgc tgc ccg ttc tct aag ggt gtg 292  
 44 Leu Thr Val Ser Gly Thr Ser Ser Cys Cys Pro Phe Ser Lys Gly Val  
 45 75 80 85 90  
 46 tct tgt ggt gat ggc tac cac tgc tgc ccc cag ggc ttc cac tgt agt 340  
 47 Ser Cys Gly Asp Gly Tyr His Cys Cys Pro Gln Gly Phe His Cys Ser

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48				95				100				105					
49	gca	gat	ggg	aaa	tcc	tgc	ttc	cag	atg	tca	gat	aac	ccc	ttg	ggt	gct	388
50	Ala	Asp	Gly	Lys	Ser	Cys	Phe	Gln	Met	Ser	Asp	Asn	Pro	Leu	Gly	Ala	
51				110				115					120				
52	gtc	cag	tgt	cct	ggg	agc	cag	ttt	gaa	tgt	cct	gac	tct	gcc	acc	tgc	436
53	Val	Gln	Cys	Pro	Gly	Ser	Gln	Phe	Glu	Cys	Pro	Asp	Ser	Ala	Thr	Cys	
54				125				130					135				
55	tgc	att	atg	gtt	gat	ggg	tcg	tgg	gga	tgt	tgt	ccc	atg	ccc	cag	gcc	484
56	Cys	Ile	Met	Val	Asp	Gly	Ser	Trp	Gly	Cys	Cys	Pro	Met	Pro	Gln	Ala	
57				140				145					150				
58	tct	tgc	tgt	gaa	gac	aga	gtg	cat	tgc	tgt	ccc	cat	ggg	gcc	tcc	tgt	532
59	Ser	Cys	Cys	Glu	Asp	Arg	Val	His	Cys	Cys	Pro	His	Gly	Ala	Ser	Cys	
60				155				160					165			170	
61	gac	ctg	gtt	cac	aca	cga	tgc	gtt	tca	ccc	acg	ggc	acc	cac	acc	cta	580
62	Asp	Leu	Val	His	Thr	Arg	Cys	Val	Ser	Pro	Thr	Gly	Thr	His	Thr	Leu	
63					175				180					185			
64	cta	aag	aag	ttc	cct	gca	caa	aag	acc	aac	agc	gca	gtg	tct	ttg	cct	628
65	Leu	Lys	Lys	Phe	Pro	Ala	Gln	Lys	Thr	Asn	Ser	Ala	Val	Ser	Leu	Pro	
66				190					195					200			
67	ttt	tct	gtc	gtg	tgc	cct	gat	gct	aag	acc	cag	tgt	ccc	gat	gat	tct	676
68	Phe	Ser	Val	Val	Cys	Pro	Asp	Ala	Lys	Thr	Gln	Cys	Pro	Asp	Asp	Ser	
69				205				210					215				
70	acc	tgc	tgt	gag	cta	ccc	act	ggg	aag	tat	ggc	tgc	tgt	cca	atg	ccc	724
71	Thr	Cys	Cys	Glu	Leu	Pro	Thr	Gly	Lys	Tyr	Gly	Cys	Cys	Pro	Met	Pro	
72				220				225					230				
73	aat	gcc	atc	tgc	tgt	tcc	gac	cac	ctg	cac	tgc	tgc	ccc	cag	gac	act	772
74	Asn	Ala	Ile	Cys	Cys	Ser	Asp	His	Leu	His	Cys	Cys	Pro	Gln	Asp	Thr	
75				235				240				245			250		
76	gta	tgt	gac	ctg	atc	cag	agt	aag	tgc	cta	tcc	aag	aac	tac	acc	acg	820
77	Val	Cys	Asp	Leu	Ile	Gln	Ser	Lys	Cys	Leu	Ser	Lys	Asn	Tyr	Thr	Thr	
78				255					260					265			
79	gat	ctc	ctg	acc	aag	ctg	cct	gga	tac	cca	gtg	aag	gag	gtg	aag	tgc	868
80	Asp	Leu	Leu	Thr	Lys	Leu	Pro	Gly	Tyr	Pro	Val	Lys	Glu	Val	Lys	Cys	
81				270				275						280			
82	gac	atg	gag	gtg	agc	tgc	cct	gaa	gga	tat	acc	tgc	tgc	cgc	ctc	aac	916
83	Asp	Met	Glu	Val	Ser	Cys	Pro	Glu	Gly	Tyr	Thr	Cys	Cys	Arg	Leu	Asn	
84				285				290					295				
85	act	ggg	gcc	tgg	ggc	tgc	tgt	cca	ttt	gcc	aag	gcc	gtg	tgt	tgt	gac	964
86	Thr	Gly	Ala	Trp	Gly	Cys	Cys	Pro	Phe	Ala	Lys	Ala	Val	Cys	Cys	Asp	
87				300				305				310					
88	gat	cac	att	cat	tgc	tgc	ccg	gca	ggg	ttt	cag	tgt	cac	aca	gag	aaa	1012
89	Asp	His	Ile	His	Cys	Cys	Pro	Ala	Gly	Phe	Gln	Cys	His	Thr	Glu	Lys	
90				315				320				325			330		
91	gga	acc	tgc	gaa	atg	ggg	atc	ctc	caa	gta	ggg	tgg	atg	aag	aag	gtc	1060
92	Gly	Thr	Cys	Glu	Met	Gly	Ile	Leu	Gln	Val	Gly	Trp	Met	Lys	Lys	Val	
93				335					340					345			
94	ata	gcc	ccc	ctc	cgc	ctg	cca	gac	cca	cag	atc	ttg	aag	agt	gat	aca	1108
95	Ile	Ala	Pro	Leu	Arg	Leu	Pro	Asp	Pro	Gln	Ile	Leu	Lys	Ser	Asp	Thr	
96				350				355						360			

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97      cct tgt gat gac ttc act agg tgt cct aca aac aat acc tgc tgc aaa 1156
98      Pro Cys Asp Asp Phe Thr Arg Cys Pro Thr Asn Asn Thr Cys Cys Lys
99      365 370 375
100     ctc aat tct ggg gac tgg ggc tgc tgt ccc atc cca gag gct gtc tgc 1204
101     Leu Asn Ser Gly Asp Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys
102     380 385 390
103     tgc tca gac aac cag cat tgc tgc cct cag ggc ttc aca tgt ctg gct 1252
104     Cys Ser Asp Asn Gln His Cys Cys Pro Gln Gly Phe Thr Cys Leu Ala
105     395 400 405 410
106     cag ggg tac tgt cag aag gga gac aca atg gtg gct ggc ctg gag aag 1300
107     Gln Gly Tyr Cys Gln Lys Gly Asp Thr Met Val Ala Gly Leu Glu Lys
108     415 420 425
109     ata cct gcc cgc cag aca acc ccg ctc caa att gga gat atc ggt tgt 1348
110     Ile Pro Ala Arg Gln Thr Thr Pro Leu Gln Ile Gly Asp Ile Gly Cys
111     430 435 440
112     gac cag cat acc agc tgc cca gta ggg caa acc tgc tgc cca agc ctc 1396
113     Asp Gln His Thr Ser Cys Pro Val Gly Gln Thr Cys Cys Pro Ser Leu
114     445 450 455
115     aag gga agt tgg gcc tgc tgc cag ctg ccc cat gct gtg tgc tgt gag 1444
116     Lys Gly Ser Trp Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu
117     460 465 470
118     gac cgg cag cac tgt tgc ccg gcc ggg tac acc tgc aac gtg aag gcg 1492
119     Asp Arg Gln His Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala
120     475 480 485 490
121     agg acc tgt gag aag gat gtc gat ttt atc cag cct ccc gtg ctc ctg 1540
122     Arg Thr Cys Glu Lys Asp Val Asp Phe Ile Gln Pro Pro Val Leu Leu
123     495 500 505
124     acc ctc ggc cct aag gtt ggg aat gtg gag tgt gga gaa ggg cat ttc 1588
125     Thr Leu Gly Pro Lys Val Gly Asn Val Glu Cys Gly Glu Gly His Phe
126     510 515 520
127     tgc cat gat aac cag acc tgt tgt aaa gac agt gca gga gtc tgg gcc 1636
128     Cys His Asp Asn Gln Thr Cys Cys Lys Asp Ser Ala Gly Val Trp Ala
129     525 530 535
130     tgc tgt ccc tac cta aag ggt gtc tgc tgt aga gat gga cgt cac tgt 1684
131     Cys Cys Pro Tyr Leu Lys Gly Val Cys Cys Arg Asp Gly Arg His Cys
132     540 545 550
133     tgc ccc ggt ggc ttc cac tgt tca gcc agg gga acc aag tgt ttg cga 1732
134     Cys Pro Gly Gly Phe His Cys Ser Ala Arg Gly Thr Lys Cys Leu Arg
135     555 560 565 570
136     aag aag att cct cgc tgg gac atg ttt ttg agg gat ccg gtc cca aga 1780
137     Lys Lys Ile Pro Arg Trp Asp Met Phe Leu Arg Asp Pro Val Pro Arg
138     575 580 585
139     ccg cta ctg taaggaaggg ctacagactt aaggaactcc acagtcctgg 1829
140     Pro Leu Leu
142     gaaccctgtt ccgagggtac ccactactca ggcctcccta gcgcctcctc ccctaacgtc 1889
143     tccccggcct actcatcctg agtcacccta tcaccatggg aggtggagcc tcaaactaaa 1949
144     accttctttt atggaaagaa ggctctggcc aaaagccccg tatcaaactg ccatttcttc 2009
145     cggtttctgt ggacctgtg gccaggtgct cttcccgagc cacaggtgtt ctgtgagctt 2069
146     gcttgtgtgt gtgtgcgcgt gtgcgtgtgt tgctccaata aagtttgtac gctttctgaa 2129

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149 <210> SEQ ID NO: 2
150 <211> LENGTH: 589
151 <212> TYPE: PRT
152 <213> ORGANISM: Mouse epithelin/granulin
153 <400> SEQUENCE: 2
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156      Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu
157           20              25              30
158      Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys Asn Pro Leu Leu Asp Thr
159           35              40              45
160      Trp Pro Arg Ile Thr Ser His His Leu Asp Gly Ser Cys Gln Thr His
161           50              55              60
162      Gly His Cys Pro Ala Gly Tyr Ser Cys Leu Leu Thr Val Ser Gly Thr
163           65              70              75              80
164      Ser Ser Cys Cys Pro Phe Ser Lys Gly Val Ser Cys Gly Asp Gly Tyr
165           85              90              95
166      His Cys Cys Pro Gln Gly Phe His Cys Ser Ala Asp Gly Lys Ser Cys
167           100             105             110
168      Phe Gln Met Ser Asp Asn Pro Leu Gly Ala Val Gln Cys Pro Gly Ser
169           115             120             125
170      Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys Cys Ile Met Val Asp Gly
171           130             135             140
172      Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg
173           145             150             155             160
174      Val His Cys Cys Pro His Gly Ala Ser Cys Asp Leu Val His Thr Arg
175           165             170             175
176      Cys Val Ser Pro Thr Gly Thr His Thr Leu Leu Lys Lys Phe Pro Ala
177           180             185             190
178      Gln Lys Thr Asn Ser Ala Val Ser Leu Pro Phe Ser Val Val Cys Pro
179           195             200             205
180      Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser Thr Cys Cys Glu Leu Pro
181           210             215             220
182      Thr Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Ile Cys Cys Ser
183           225             230             235             240
184      Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile Gln
185           245             250             255
186      Ser Lys Cys Leu Ser Lys Asn Tyr Thr Thr Asp Leu Leu Thr Lys Leu
187           260             265             270
188      Pro Gly Tyr Pro Val Lys Glu Val Lys Cys Asp Met Glu Val Ser Cys
189           275             280             285
190      Pro Glu Gly Tyr Thr Cys Cys Arg Leu Asn Thr Gly Ala Trp Gly Cys
191           290             295             300
192      Cys Pro Phe Ala Lys Ala Val Cys Cys Asp Asp His Ile His Cys Cys
193           305             310             315             320
194      Pro Ala Gly Phe Gln Cys His Thr Glu Lys Gly Thr Cys Glu Met Gly
195           325             330             335
196      Ile Leu Gln Val Gly Trp Met Lys Lys Val Ile Ala Pro Leu Arg Leu

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2137

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197          340          345          350
198  Pro Asp Pro Gln Ile Leu Lys Ser Asp Thr Pro Cys Asp Asp Phe Thr
199          355          360          365
200  Arg Cys Pro Thr Asn Asn Thr Cys Cys Lys Leu Asn Ser Gly Asp Trp
201          370          375          380
202  Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp Asn Gln His
203  385          390          395          400
204  Cys Cys Pro Gln Gly Phe Thr Cys Leu Ala Gln Gly Tyr Cys Gln Lys
205          405          410          415
206  Gly Asp Thr Met Val Ala Gly Leu Glu Lys Ile Pro Ala Arg Gln Thr
207          420          425          430
208  Thr Pro Leu Gln Ile Gly Asp Ile Gly Cys Asp Gln His Thr Ser Cys
209          435          440          445
210  Pro Val Gly Gln Thr Cys Cys Pro Ser Leu Lys Gly Ser Trp Ala Cys
211          450          455          460
212  Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His Cys Cys
213  465          470          475          480
214  Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Thr Cys Glu Lys Asp
215          485          490          495
216  Val Asp Phe Ile Gln Pro Pro Val Leu Leu Thr Leu Gly Pro Lys Val
217          500          505          510
218  Gly Asn Val Glu Cys Gly Glu Gly His Phe Cys His Asp Asn Gln Thr
219          515          520          525
220  Cys Cys Lys Asp Ser Ala Gly Val Trp Ala Cys Cys Pro Tyr Leu Lys
221          530          535          540
222  Gly Val Cys Cys Arg Asp Gly Arg His Cys Cys Pro Gly Gly Phe His
223  545          550          555          560
224  Cys Ser Ala Arg Gly Thr Lys Cys Leu Arg Lys Lys Ile Pro Arg Trp
225          565          570          575
226  Asp Met Phe Leu Arg Asp Pro Val Pro Arg Pro Leu Leu
227          580          585
229 <210> SEQ ID NO: 3
230 <211> LENGTH: 19
231 <212> TYPE: PRT
232 <213> ORGANISM: mouse granulin
233 <220> FEATURE:
234 <221> NAME/KEY: PEPTIDE
235 <222> LOCATION: (1)..(19)
236 <223> OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
237      antisera against the GP88 used in the
238      immunoaffinity step.
239 <400> SEQUENCE: 3
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241      1          5          10          15
242      Ser Asp Thr
244 <210> SEQ ID NO: 4
245 <211> LENGTH: 12
246 <212> TYPE: PRT
247 <213> ORGANISM: mouse granulin

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## VERIFICATION SUMMARY

DATE: 03/19/2002

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Output Set: N:\CRF3\03192002\I824647.raw

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L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
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